

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 3, 2002, 23:27:20 ; Search time 45.2264 Seconds
(without alignments)
1084.239 Million cell updates/sec

Title: US-09-805-550-4
Perfect score: 1910
Sequence: 1 MRLTYKTKGTFETRVQPN.....CORNEELANYLLEHAGEED 368

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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23: /SID2/gcgdata/geneseq/emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1910	100.0	368	21	AA171459
2	1169.5	58.4	371	21	AA17377
3	1115	55.9	368	21	AA17378
4	1067.5	53.1	348	21	AA17378
5	1014	53.1	345	21	AA17378
6	931.5	48.8	378	21	AA17378
7	931.5	48.8	378	21	AA17378
8	900.5	47.1	405	21	AA17378
9	871.5	45.6	289	21	AA17378
10	834	43.7	335	21	AA17378

11	834	43.7	335	21	AA17378	Arabidopsis thalia
12	820	42.9	286	21	AA17378	Arabidopsis thalia
13	742	38.8	307	21	AA17378	Arabidopsis thalia
14	742	38.8	307	21	AA17378	Arabidopsis thalia
15	634	33.2	416	23	AA17378	Mouse ischaemic co
16	622.5	32.6	409	19	AA17378	Vpr protein bindin
17	622.5	32.6	409	19	AA17378	Vpr protein bindin
18	604	31.6	117	23	AA17378	Human ORF3591 prot
19	603.5	31.6	363	18	AA17378	E6AP-binding prote
20	603.5	31.6	363	19	AA17378	Vpr protein bindin
21	603.5	31.6	363	19	AA17378	Vpr binding protei
22	603	31.6	379	21	AA17378	Breast and ovarian
23	574.5	30.1	346	18	AA17378	Nuclear mitotic ap
24	563.5	29.5	257	21	AA17378	Arabidopsis thalia
25	487.5	25.5	414	22	AA17378	Drosophila melanog
26	466	24.4	214	21	AA17378	Arabidopsis thalia
27	375	19.6	290	22	AA17378	Drosophila melanog
28	374	19.6	186	21	AA17378	Arabidopsis thalia
29	356	18.6	179	19	AA17378	Vpr protein bindin
30	356	18.6	179	19	AA17378	Vpr binding protei
31	333	17.4	174	19	AA17378	Protein sequence o
32	333	17.4	174	19	AA17378	Protein sequence o
33	308.5	16.2	136	21	AA17378	Arabidopsis thalia
34	292.5	15.3	150	19	AA17378	Protein sequence o
35	292.5	15.3	150	19	AA17378	Protein sequence o
36	217	11.4	112	19	AA17378	Human 1492H#151 u
37	217	11.4	112	19	AA17378	Human SAP2 amino a
38	195.5	10.2	536	21	AA17378	Human protease and
39	195.5	10.2	577	21	AA17378	Novel human diagno
40	182	9.5	79	20	AA17378	Ubiquitin-like dom
41	177	9.3	589	22	AA17378	Human protein sequ
42	176	9.2	464	21	AA17378	Human 1492H#151 u
43	176	9.2	589	22	AA17378	Human SAP2 amino a
44	176	9.2	589	22	AA17378	Human protease and
45	176	9.2	604	22	AA17378	Novel human diagno

ALIGNMENTS

RESULT 1
ID AA171459 standard; Protein: 368 AA.
XX AA171459;
AC AA171459;
XX 04-OCT-2000 (first entry)
DE Maize Rad23 protein #2.
KW Rad23; maize; ATCC No: PTA-531; recombinant expression cassette; wheat;
KW transgenic plant; soybean; sunflower; sorghum; canola; modulator.
XX
OS Zea mays.
XX
PN WO200031268-A1.
XX
PD 02-JUN-2000.
XX
PF 12-OCT-1999; 99WO-US24129.
XX
PR 23-NOV-1998; 98US-0109728.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Mahajan PB, Tagliani L;
XX WPI; 2000-400078/34.
XX N-PSDB; AAD01231.
XX
PT Isolated nucleic acid encoding maize RAD23 protein is used to modulate
PT the levels of polypeptides in plant or in assays for identifying
PT compounds that bind to and/or increase/decrease enzymatic activity of

PT catalytically active polypeptides -
XX
PS Claim 11b; Page 78-79; 82pp; English.
XX
CC The present sequence is the maize Rad23 protein #2. It is isolated from
CC a Zea mays cell line, B73 callus tissue regenerated five days after
CC transfer of the callus from medium containing auxin to a medium devoid
CC of exogenous auxin. The cDNA is deposited under the ATCC No: PTA-531.
CC Maize Rad23 DNA sequence operably linked to a promoter, can be used to
CC construct a recombinant expression cassette. This expression cassette
CC can be used to generate a dicot or monocot transgenic plant e.g., maize,
CC soybean, sunflower, sorghum, canola, wheat, etc.. It can also be used to
CC modulate the levels of Rad23 polypeptide expression in a plant or in
CC assays to identify compounds, that bind to and/or modulate the enzymatic
CC activity of catalytically active polypeptides.
XX
SQ Sequence 368 AA:

Query Match 100.0%; Score 1910; DB 21; Length 368;
Best Local Similarity 100.0%; Pred. No. 7,6e-147;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLTYVTKTGFHEIRVQNDTIMAVKKNIEIIOGKDSYPMGOQLIFNGKYLKDESTLE 60
DB 1 MLTYVTKTGFHEIRVQNDTIMAVKKNIEIIOGKDSYPMGOQLIFNGKYLKDESTLE 60
QY 61 ENKVNEDGFLVYVMSKSGTSGTSSQHSMT PATROAPPLPAPQAPQAPVAPITTSQ 120
DB 61 ENKVNEDGFLVYVMSKSGTSGTSSQHSMT PATROAPPLPAPQAPQAPVAPITTSQ 120
QY 121 PEGLRQAQANTNDNASNLISGRNDITINQLEMGGSGMDKQORALRAAYNNPERAV 180
DB 121 PEGLRQAQANTNDNASNLISGRNDITINQLEMGGSGMDKQORALRAAYNNPERAV 180
QY 181 EYLYSGIPYTAIEAVPIGSGANTTDRAPTGAGLSGINTAPLIDFPGASNAGGAGG 240
DB 181 EYLYSGIPYTAIEAVPIGSGANTTDRAPTGAGLSGINTAPLIDFPGASNAGGAGG 240
QY 241 GPLDFLRNNPQFQAVREWHVNPQILQPLVLSKONPQILRIEHNDEFIQLNEPPE 300
DB 241 GPLDFLRNNPQFQAVREWHVNPQILQPLVLSKONPQILRIEHNDEFIQLNEPPE 300
QY 301 GGEQDFLOPDEDEPHALSYTPEQOATGRLESKGFDAARYTEAFACDRNEELANTL 360
DB 301 GGEQDFLOPDEDEPHALSYTPEQOATGRLESKGFDAARYTEAFACDRNEELANTL 360
QY 361 LEHAGEED 368
DB 361 LEHAGEED 368

RESULT 2
AAG17377
ID AAG17377 standard; Protein; 371 AA.
AC AAG17377;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18372.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX

PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
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Query Match 61.28; Score 1169.5; DB 21; Length 371;
Best Local Similarity 64.38; Pred. No. 1.1e-86;
Matches 247; Conservative 43; Mismatches 65; Indels 29; Gaps 9;

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DB 1 MKLIVKTLKGSFHEIRVLPDPTIMAVKKNIEDSGKDNYPGQOLLHNGKVLKDESTLV 60
QY 61 ENKVNEDGFLVYMLSKGTSGTSSQSHN-----TPATROAPPLERAPQAPPP 112
DB 61 ENKVTBEGFLVYMLSKSGSAGQASVQTSVQPYSATTSSTKPAAP--STQSSPY 118
QY 113 VAPITTSQPEGLPAQAPTHNNAASNLISGRNVDTIINQLMKGGSKDKVORALRA 172
DB 119 ASPIPAQEQ---PAQIDTYGQAASVLYSGSSLSQMVQOIMEMGGSKDKETVTRALRA 175
QY 173 YNNPERAVEYLYSGIPYTAETFAVP-----IGGOGANTTDRAPTGEBAGISGTPNTAPLDLF 227
DB 176 YNNPERAVDYLYSGIPYTAETFAVPPEQAQAGSGA-----APVAPA--SGSPNSPDLF 228
QY 228 POGASNAGGAGGGLDFLRNNPOFAVRENVHTNPOTIQPLVELSKONFOILRIEEN 287
DB 229 PQETVVAAGSGDLGLTELRNNDOFQQLRWVHSPQLQPMLEIGLQNNQLRLIOEN 288
QY 288 HDEFLQLINEPPEG--GGGDLDPDEDEMPHAISVTPEDQDAIGRLSKGFDARVIEA 345
DB 289 QAELFLOLVNEPEYEGSDGDMFDQPEQ-EMPHAINVPAEQDAIORLEAMGFDRAVIEA 347
QY 346 FLACDRNEELANYLLEHAGE-ED 368
DB 348 FLACDRNEELANYLLENSGDFED 371
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XX AC AAG44341;

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PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
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PR 07-SEP-1999; 99US-0152363.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 58.4%; Score 1115; DB 21; Length 368;
Best Local Similarity 62.8%; Pred. No. 2.9e-62;
Matches 235; Conservative 45; Mismatches 82; Indels 12; Gaps 8;

QY 1 MKLTVKTKLSTKFEIRVQPDITIMAVKNIETIQKSDYPMGQOOLLFNGKVLKDEESTLE 60
DB 1 MKLTVKTKLSTKFEIRVLPDITIMAVKNIETIQKSDYPMGQOOLLFNGKVLKDEESTLE 60
QY 61 ENKYNEDGFLVMSKSKTSGTGTSSQ-HSNTPATROAPLEAPQADPPVAPITTS 119
DB 61 ENKYNEDGFLVMSKSKTSGTGTSSQ-HSNTPATROAPLEAPQADPPVAPITTS 119
QY 120 QP-EGLPAPAPNTHDNASNLSCRNVDITIIINOLMEMGGSGWDKXORALRAAYNNPER 178
DB 120 TPVOEOPTPASDITYGQALASTLVSSSTEQWQOITMEMGGSGWDKXORALRAAYNNPER 178
QY 179 AVEYLXSGIVPTAEI-AVPIGGGAGANTTDRAPTGEAGLISGIPNTAPLDFPQAGASNAGCG 237
DB 180 AVDYLVSGIETVYIPATNLSGVSGRELTAAPP---SSGPNSSPLDLPQAEAVSDAG 235
QY 238 AGGGPLDFLKNNPQFAVREKHTNPQIILQPMVELSKNPQIILRIENHDEFLQLINE 297

DB 236 GDLGTLEFLKRGNDQFOQLRSWVNSNPQILOPMLOELKONPQILRLIQENQAEFLQLINE 295
QY 298 PFECEGEC--DFLDQPEDEMDHAISVTPPEROEATIGRLSNGFDRARYIEAFIACDRNEEL 355
DB 296 PYESGDGVDIFDPQDQ-EMPHSVNVTPEQESIERLEAMGFDAIYIEAFISCDRNEEL 354
QY 356 AANYLLEHAGE-ED 368
DB 355 AANYLLEHAGE-ED 368
RESULT 4
AAG17378
ID AAG17378 standard; Protein; 348 AA.
XX
AC AAG17378;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 18373.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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PR	09-JUL-1999;	9905-0142820;
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PR	15-SEP-1999;	9905-0154018
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PR	25-OCT-1999;	9905-0161405
PR	25-OCT-1999;	9905-0161406
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PR	26-OCT-1999;	9905-0161361
PR	28-OCT-1999;	9905-0161920
PR	28-OCT-1999;	9905-0161920
PR	29-OCT-1999;	9905-0161993
PR	29-OCT-1999;	9905-0162142

Query Match	48.8%;	Score 931.5;	DB 21;	Length 378;
Best Local Similarity	52.6%;	Pred. No. 2.4e-67;		
Matches 200;	Conservative 56;	Mismatches 109;	Indels 15;	Gaps 8

[illegible]

DB 358 NKNNEIAANYLDHMHFEFD 377

RESULT 8
AAV71458
ID AAV71458 standard; Protein; 405 AA.
XX AAV71458;
AC AAV71458;
XX
XX 04-OCT-2000 (first entry)
DT
XX
XX
DE Maize Rad23 protein #1.
XX
XX Rad23; maize; ATCC No: PTA-530; recombinant expression cassette; wheat;
KM transgenic plant; soybean; sunflower; sorghum; canola; modulator.
XX
OS Zea mays.
XX
XX WO200031268-A1.
PN
XX 02-JUN-2000.
PD
XX 12-OCT-1999; 99WO-US24129.
XX
XX 23-NOV-1998; 98US-0109728.
XX
XX (PION-) PIONEER HI-BRED INT INC.
PA
XX
XX Mahajan PB, Tagliant L;
PI
XX
XX WPI: 2000-400078/34.
DR N-PSDB: AAD01230.
XX
XX
XX Isolated nucleic acid encoding maize RAD23 protein is used to modulate
PT the levels of polypeptides in plant or in assays for identifying
PT compounds that bind to and/or increase/decrease enzymatic activity of
PT catalytically active polypeptides -
XX
XX
XX Claim 11b; Page 75-76; 82pp; English.
XX
XX The present sequence is the maize Rad23 protein #1. It is isolated from
CC v5 root tissue of a Zea mays cell line B73, infested with corn root
CC worm. The cDNA sequence is deposited under the ATCC No: PTA-530. Maize
CC Rad23 DNA sequence operably linked to a promoter can be used to construct
CC a recombinant expression cassette. This expression cassette can be used
CC to generate a dicot or monocot transgenic plant e.g., maize, soybean,
CC sunflower, sorghum, canola, wheat, etc.. It can also be used to modulate
CC the levels of Rad23 polypeptide expression in a plant or in assays to
CC identify compounds, that bind to and/or modulate the enzymatic activity
CC of catalytically active polypeptides.
XX
XX
SQ Sequence 405 AA;
Query Match 47.1%; Score 900.5; DB 21; Length 405;
Best Local Similarity 49.0%; Pred. No. 8,7e-65;
Matches 197; Conservative 53; Mismatches 117; Indels 35; Gaps 7;
QY 1 MRLTVKTLKGFHEIRVQNDTIAVKNKIEIOGKDYPMGOQLIENGKYLKDESTLE 60
DB 1 MRLNKTTLKGTFFELASDASVADYKRITETGOSTYRADQOMLITGKLIKDETTLE 60
QY 61 ENKVEDGFLVVMLSKGTSGTSSQSHSTPATRQAP-----PLEAPQAP-OPPYA 114
DB 61 SNGVAVENSLVYMLSKAKAS-SSGASTATTAKAPATLQAPAPVAPASVARTPTQAPYA 119
QY 115 PITTSQPEBLPAQAP-----NTHNMA SNLISGNVVTIINOLMEKSGSMDKDK 164
DB 120 TAEITAPPSYQPAAPATVATDDADVISOAASNIVFGNNLISQTLIOQLIDMGGTWERDY 179
QY 165 VQALRAAYNNDEBAVEYLSGIPYTAE----IAVPIGGOGANTTDRAPTGEA----- 213
DB 180 VYRAIRAAVNNRERADITVYSGIPENVEAQPARAPAGQGNQQAASPAQPAVALPVP 239

QY 214 -GLSGIPNTAPLDLPFGASNMAG-----GAGGGLDFLRNNPOFAVREWHNPQIL 266
DB 240 SPASAGPNANPLNLFPGVSGSGSNPGVYVAGSGALDRLRQIPORALLQIVQANPQIL 299
QY 267 QPMLVELSKONPQILRLIENHDEFIOLLNPEPGESEDFLOQPEDEKPHNISTVPEEQ 326
DB 300 QPMLQELGKONPQILRLIDENQAEPLRLVNESPEGGPGGNILGQLAAAPQTLTVPEER 359
QY 327 EAIGRLSEMGFDRARYTEAFACDRNEELAAANYLEHAGEED 368
DB 360 EATQRLGEMGFNRELYLEVFPACNKRDELLFANYLDHGHFEFD 401

RESULT 9
AAG17379
ID AAG17379 standard; Protein; 299 AA.
XX
XX AAG17379;
AC
XX
XX 17-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 18374.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
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XX 25-FEB-1999; 99US-0121825.
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PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131048.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-01332407.
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PR 04-JUN-1999; 99US-0137502.

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PR 29-OCT-1999; 99US-0162142.

Query Match 43.7%; Score 834; DB 21; Length 335.
Best Local Similarity 53.3%; Pred. No. 1,7e-59;
Matches 179; Conservative 47; Mismatches 96; Indels 14; Gaps 7;

QY 45 LLIENGKVLKDESTLEENKVNEDGFLVYMLSKGKTS---GSTGTSSSHSMTPATROAP 101
DB 1 MLIHGKVLKDETLLEENNVENSPIVIMLSKTRASPGCASTASAPASAIQPTVATPQ 60

QY 102 LEAP-QQAPPPVAPITTSQPEGLPAQAPNTHDNASNLSGRNYDTIINQLEMKGGSW 160
DB 61 VSAPFASVPVPTSGTATAAPATAASVQTDVYQGAASMLVAGTTLSTVQQLIDMGGSW 120

QY 161 DKDKYQRLRAAYNNPERAVETLYSGITVTAET-----AVPIGGOGAN--TTDRAPGEA 213
DB 121 DDDTVRALRAAFNNPERAVETLYSGIPAOAIEPPVQAAPTGEQANPLAQPOQAAPA 180

QY 214 GLSGIPNPAFLDPEOGASNAGGAGGAPLDLFRNNPOFOAVREVVHNPQIOLMIVEL 273
DB 181 AATGGNANPLNLPFGQAPADAGAGNLDPLRNSQOFQAIRAVQANPOLLOPMLOEL 240

QY 274 SKQNPQILRIEENHDEFLOLNEPFEGBEGDLDQPEDEMPHAISVTPPEQEAIGRL 333
DB 241 GKQNPQILRIEENHDEFLOLNEPFEGBEGDLDQPEDEMPHAISVTPPEQEAIGRL 298

QY 334 SMGPDRAVITAEFLACDNRRELAANYLLEHAGE-ED 368
DB 299 GMGPDRAVITAEFLACDNRRELAANYLLEHAGE-ED 334

RESULT 11
AAG45205
ID AAG45205 standard; Protein: 335 AA.
XX
AC AAG45205;
XX
DT 18-Oct-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 56724.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
PN EP1033405-A2.
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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PR 18-OCT-1999; 99US-0159584.
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PR 21-OCT-1999; 99US-0160767.
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PR 28-OCT-1999; 99US-0161920.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 43.7%; Score 834; DB 21; Length 335;
Best Local Similarity 53.3%; Pred. No. 1,7e-59;

Matches 179; Conservative 47; Mismatches 96; Indels 14; Gaps 7;

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OY 102 LEAP-QQAPQPPVAPITTSOPEGLPAQAPNTHDNAASMLSGRVDTITNOJMEMGGSW 160
DB 61 VSAFTASVPVTSSTGATAAAPTAAASVQTQVYQQAASLVAGTLESTVQOITLDMGGSW 120
OY 161 DKDVQALRAAYNNPERAVYILSGIPVTAET----AVIGGOGAN--TTDRAPIGE 213
DB 121 DRDTVVALRLRAFNPPRAAYVYLSGIPQAQEIPPVAQAPRTGQAANPLAOPQAAAPA 180
OY 214 GLSGIPTAPLDFLPQGSASNAGGAGGGLDFLRNNPOFAVREKVAHNPQILOPMLVEL 273
DB 181 AATGPPANPLNLPQGPAPADAGAGAGNLDPLRNSQOFLIRAVQANPQILOPMLQEL 240
OY 274 SKQNPQILRLIEENHDEFLQLNPFEGEGDFLDQPEDEMPHAISVTPREOARIGLE 333
DB 241 GKQNPQVRLIQEHQADFLRLINEPVE-GEENVMEQLQA-AMPQAVTYTPEREALIELE 298
OY 334 SMGDFRARVITAFACDRNELANYLEHAGE-ED 368
DB 299 GMGFDRAVMLEVFPACNKNELANYLEHMEFEED 334

RESULT 12

AAG44343
ID AAG44343 standard; Protein; 296 AA.

AC AAG44343;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 55533.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

PN EPI033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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Query Match	42.9%	Score 820	DB 21	Length 256
Best Local Similarity	58.3%	Pred. No. 2e-56		
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 21983.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-030139.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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Query Match 38.8%; Score 742; DB 21; Length 307;

Best Local Similarity 52.3%; Pred. No. 4.5e-52;

Matches 161; Conservative 42; Mismatches 91; Indels 14; Gaps 7;

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DB 61 TDVYGOAASNLVAGTTLSTEQIILDMGGSWDRTVVRALRAAENPRAVEYLYSGIP 120
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DB 121 AOAETPPVAQAAPATGEQAANPLAOPQOAAAPAAATGGPVANPLNLFPGMPAADAGAGAG 180
QY 242 PLUDEFRRNPQFAVREMYHTNPQIOLPMLVETSKONPOLIRLENNHDEFQLLNEPFG 301
DB 181 NUDFLRNQOQALRAMQOANQIILPMLDELGKONPOLVRLIQHQADFLLINEPVE- 239
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RESULT 14
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AC AAG45206;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 56725.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
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Query Match 38.8%; Score 742; DB 21; Length 307;
Best Local Similarity 52.3%; Pred. No. 4,5e-52;
Matches 161; Conservative 42; Mismatches 91; Indels 14; Gaps 7;

OY 73 MLSKGTSTSGTGSSSHSNTPATROAPLEAP-OQAPQPPVADITTSQPEGILPAQA 128
Db 1 MLSKTKASPSGASTASAPASATQPQTATPQVSAPRASVPPTSATATAAATAASVQ 60
OY 129 PNTIDNAAUNLISGRNDDTIINQLEMGGSGWCKDKQRLRAAYNNPERAVEYLYGIP 188
Db 61 TDYVGAASNLVAGTTTSTVVOQILDMGGSGWDRDITVVRALRAAFNNPERAVEYLYGIP 120

QY 189 VTAET-----AVPIGGGAG--TTDRAPTGEAGLSGIPNTAPLDLFPQGASNAGCGAGG 241
DB 121 AQAETPVAQAAPATGEOQANPLAQPOQAAPAAATGAGNANLNFPOGMPAADGAGAG 180
QY 242 FLDFLRNPOFOAVREHTNPQILQPMVLVELSKONPOLRIEENHDEFQLLNEPEG 301
DB 181 NLDFLRNCOFOALRAMYQANPQILQPMVLGKONPOLVRLIQHQADEFRLINEPEV- 239
QY 302 GEGDFLDQPEDEMPHAISVPEEQEAGIRLESNGFDRARYEAFLACDRNEELANYLL 361
DB 240 GEEVMEQLEA-AMPQAVTVPEEREALIERLEGMGFDRAMYLEVFACNKNELANYLL 298
QY 362 EHAG-ED 368
DB 299 DHMEFED 306

RESULT 15
ABB57171
ID ABB57171 standard; Protein: 416 AA.
AC ABB57171;
XX 07-MAR-2002 (first entry)
DE Mouse ischaemic condition related protein sequence SEQ ID NO:415.
XX
KW Mouse; Ischaemia; compressive ischaemia; occlusive ischaemia;
KV vasospastic ischaemia; ischaemic condition; ischaemic disease.
OS Mus musculus.
PN W020018188-A2.
PD 22-NOV-2001.
PF 18-MAY-2001; 2001WO-JP04192.
XX
PR 18-MAY-2000; 2000JP-0145977.
XX
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
DR WPI: 2002-034733/04.
DR N-PSDB: ABI99464.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -
XX
XX Claim 2; Page 1132-1134; 2690pp; English.
XX
CC The present invention describes a method for examining ischemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912), encoding
CC the protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischemic condition-improving
CC drugs or therapeutics for ischemic diseases. ABI99913 and ABI99914
CC represent PCR primers for a mouse ischaemic condition related sequence,
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 416 AA;

Query Match 33.2%; Score 634; DB 23; Length 416;

Best Local Similarity 33.5%; Pred. No. 4e-43;
Matches 146; Conservative 93; Mismatches 109; Indels 88; Gaps 11;
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DB 1 MGVTLKTIQQQFFKIDIDPEETVKALKKEISEKCKDAFPVAGOKLIYAGKLSLSDYALK 60
QY 61 ENKVNEDGFLVYMLSKGTSGSTSSQHSNTPA---TROAPLEAPQ-QAPQPPVAPT 116
DB 61 EKKIDEKNVVVVMYKPAVTVAPATTOPSSPTTVSSPVAVAAQAPAPFPALAPT 120
QY 117 TT-----SOPE---GLPAPQAP-----NTHNA 135
DB 121 STPASTTPASTTASSEPAACATQPEKPAEKPAQTPVLTSPAPADSTPGDSSRSNLFEDA 180
QY 136 ASNLISGRNVDITIIQLMEMGGSDKDKYORALRAAYNPERAVEYLYSGIPYTAETAV 195
DB 181 TSALVTGOSYEMMYEIMSMG---YERQVYLAALRASFNPNPRAVEYLLMGIPGDRBSQA 237
QY 196 PIGGCGANTTDRAPTGEAGLSGIPNTAPLDLFPQGASNAG-----GGAGGGLDFLRN 248
DB 238 VVD-----PPQAVSTGTQPS-----PAVAAAAATTATTGSGHPLEFLRN 281
QY 249 NPOQAVREMYHTNPQILQPMVLVELSKONPOLRIEENHDEFQLLNEPE----- 300
DB 282 QPQFOQMKQIIOQNPSLIPALIQIGRENPOLQOISQOEHFIQMLNEPVQEAGCGGCG 341
QY 301 -----GEGDFLDQPEDEMPHAISVPEEQEAGIRLESNGFDRARYEAFLACDRN 352
DB 342 GGGGGGGGGGGGGGGAIEAGSGHMN-IGVTQEKRAIRLALGPRBEVLVQAYACCKN 400
QY 353 BELANYLLERHAGEED 368
DB 401 BELANFLQQNFDED 416

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